Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 11:44:25

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524585.sorted.bam -c -nw 400 -hm 3
```

1.2. Alignment

Command line:	/home/luna/Desktop/Software/bwa/bwa mem -t 16 -k 30 -R @RG\tID:Singlecell2022\tLB:Library\tPL:ILLUMINA\tSM:sample_SRR10524585 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524585.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 11:44:24 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524585.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,919,652
Mapped reads	1,766,167 / 92%
Unmapped reads	153,485 / 8%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	8,654 / 0.45%
Read min/max/mean length	30 / 76 / 76.15
Duplicated reads (estimated)	83,562 / 4.35%
Duplication rate	3.67%
Clipped reads	1,772,893 / 92.35%

2.2. ACGT Content

Number/percentage of A's	25,519,928 / 24.76%
Number/percentage of C's	18,625,939 / 18.07%
Number/percentage of T's	32,025,873 / 31.07%
Number/percentage of G's	26,899,637 / 26.1%
Number/percentage of N's	1,494 / 0%
GC Percentage	44.17%

2.3. Coverage

Mean	0.0333

Standard Deviation	0.2918

2.4. Mapping Quality

Mean Mapping Quality	45.11

2.5. Mismatches and indels

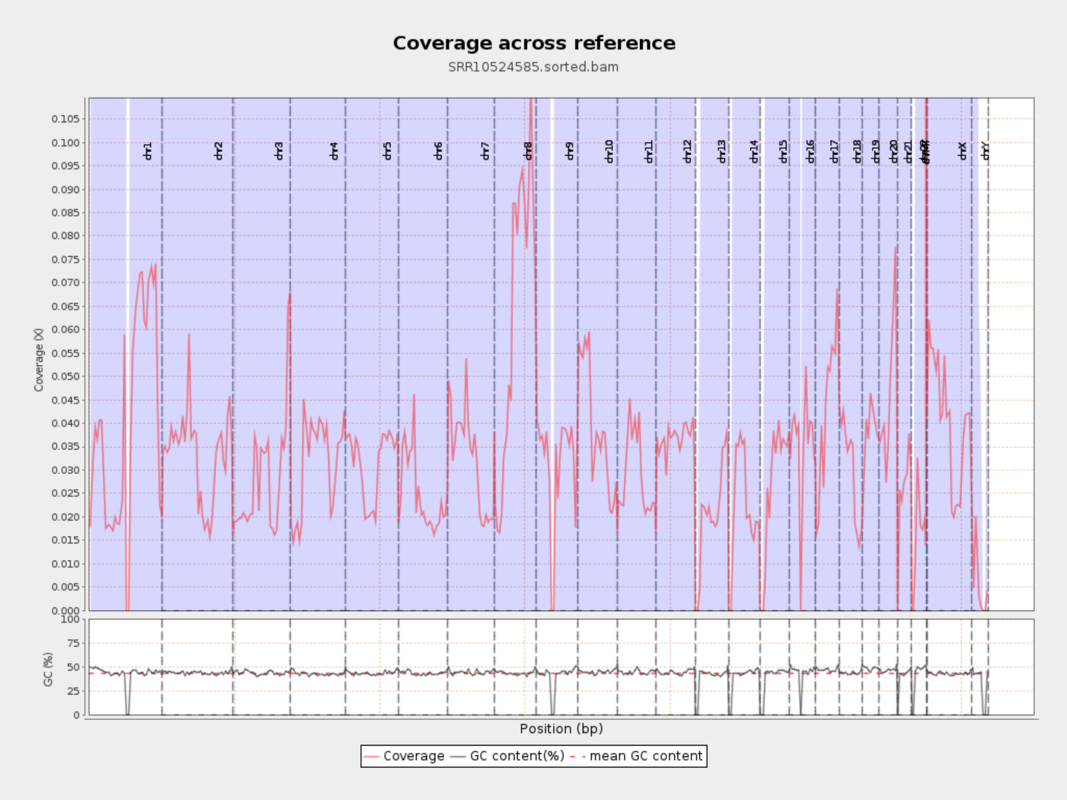
General error rate	0.51%
Mismatches	510,220
Insertions	5,488
Mapped reads with at least one insertion	0.31%
Deletions	18,064
Mapped reads with at least one deletion	1.02%
Homopolymer indels	44.74%

2.6. Chromosome stats

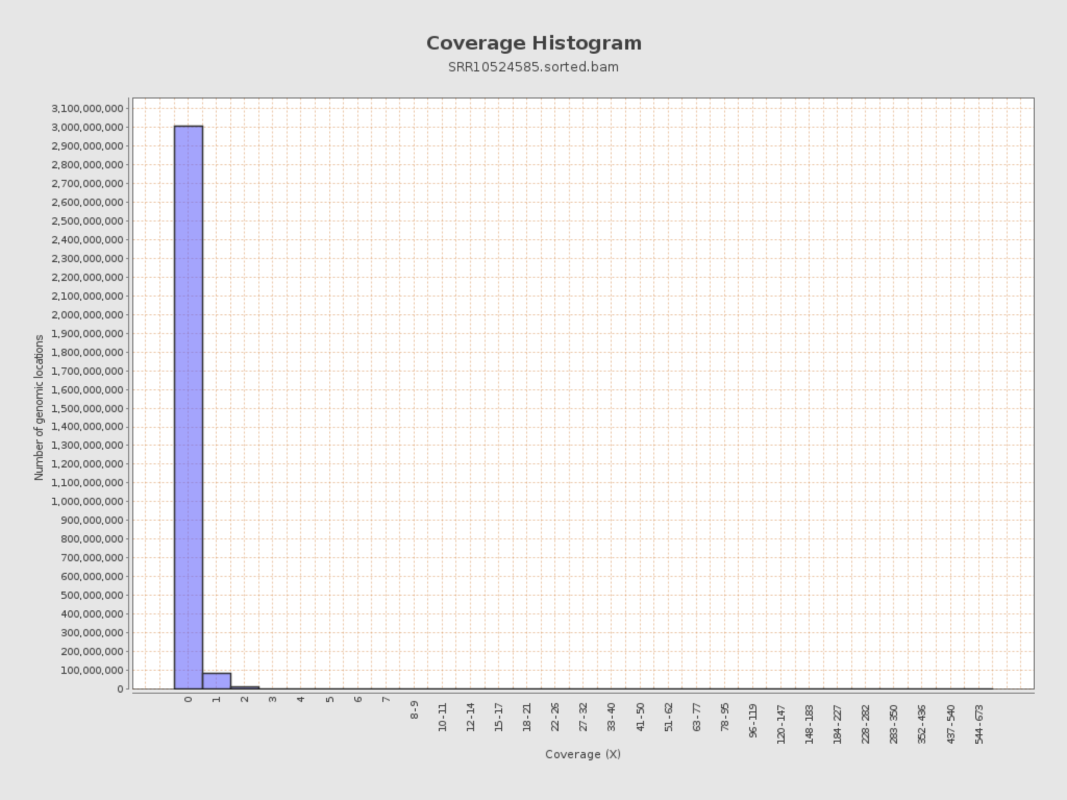
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	10039208	0.0403	0.5269
chr2	243199373	8149950	0.0335	0.3387
chr3	198022430	5451881	0.0275	0.186
chr4	191154276	6023389	0.0315	0.223
chr5	180915260	5686746	0.0314	0.1994
chr6	171115067	4230247	0.0247	0.2344
chr7	159138663	5164267	0.0325	0.3439

chr8	146364022	9319834	0.0637	0.3332
chr9	141213431	4318889	0.0306	0.2553
chr10	135534747	5332853	0.0393	0.3056
chr11	135006516	3921711	0.029	0.272
chr12	133851895	4922845	0.0368	0.2162
chr13	115169878	2394899	0.0208	0.1601
chr14	107349540	2379727	0.0222	0.1709
chr15	102531392	2729104	0.0266	0.1846
chr16	90354753	3182049	0.0352	0.22
chr17	81195210	3556517	0.0438	0.2516
chr18	78077248	2362794	0.0303	0.4315
chr19	59128983	2266254	0.0383	0.3709
chr20	63025520	2948883	0.0468	0.2463
chr21	48129895	1257714	0.0261	0.2037
chr22	51304566	791577	0.0154	0.1385
chrMT	16571	24635	1.4866	1.5153
chrX	155270560	6310094	0.0406	0.2488
chrY	59373566	336899	0.0057	0.171

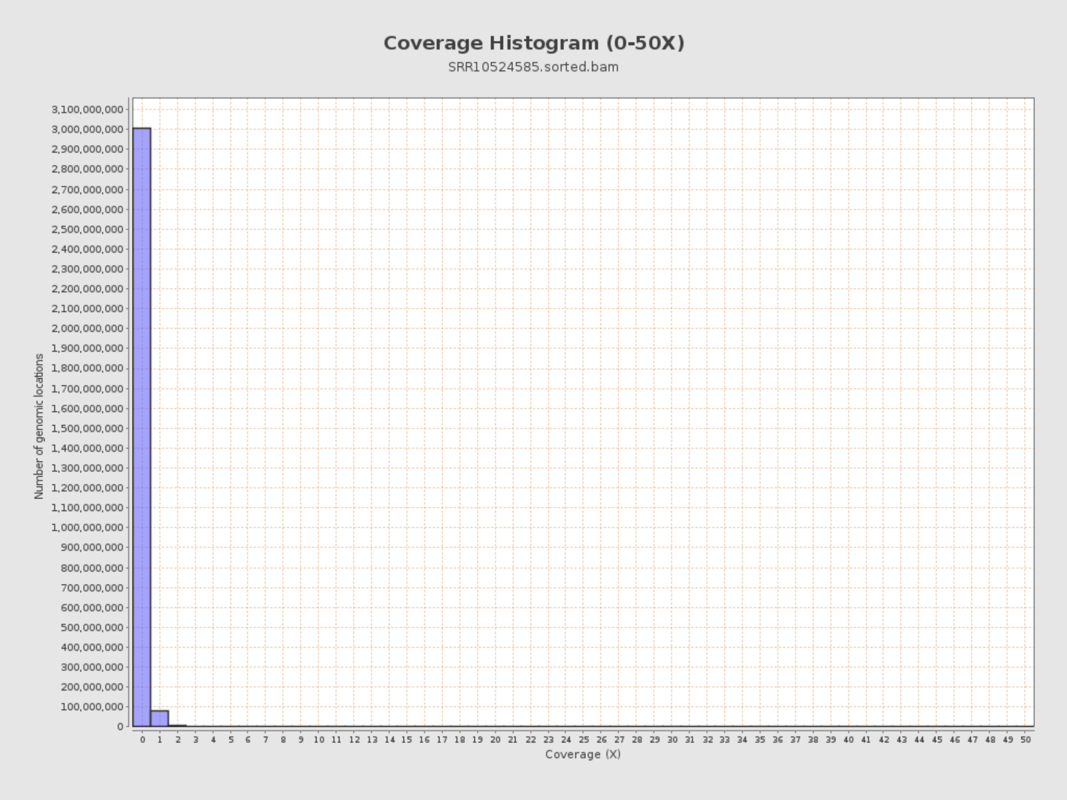
3. Results : Coverage across reference



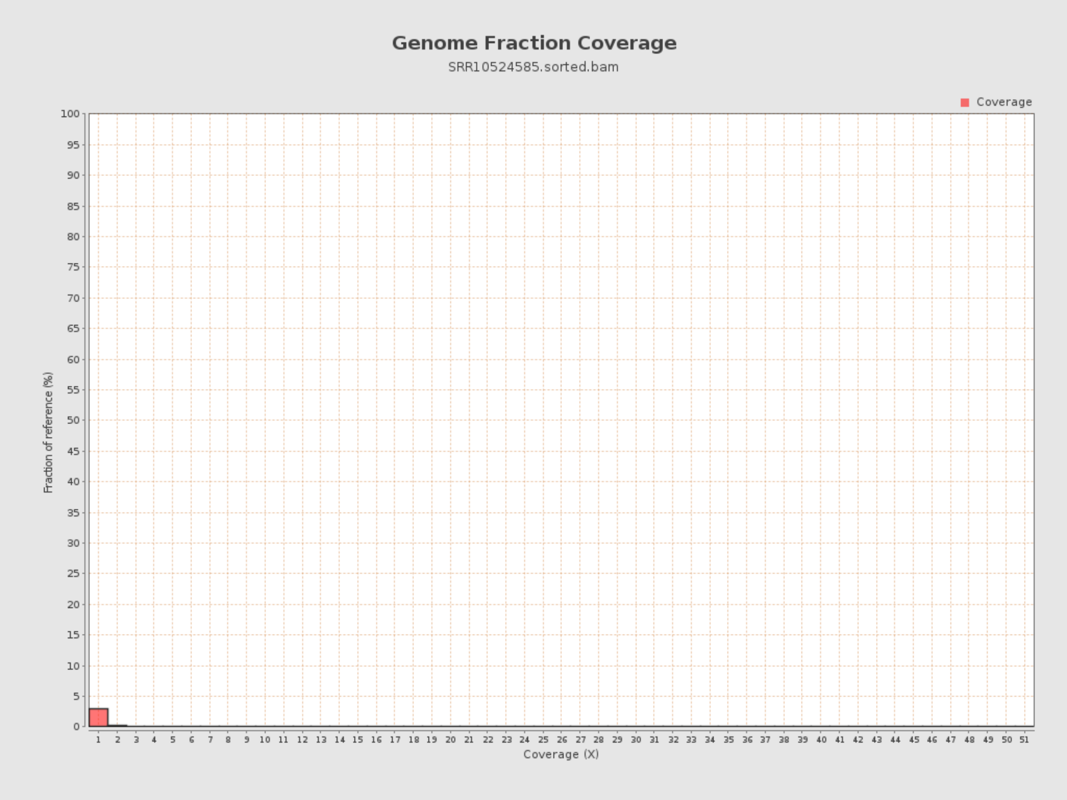
4. Results : Coverage Histogram



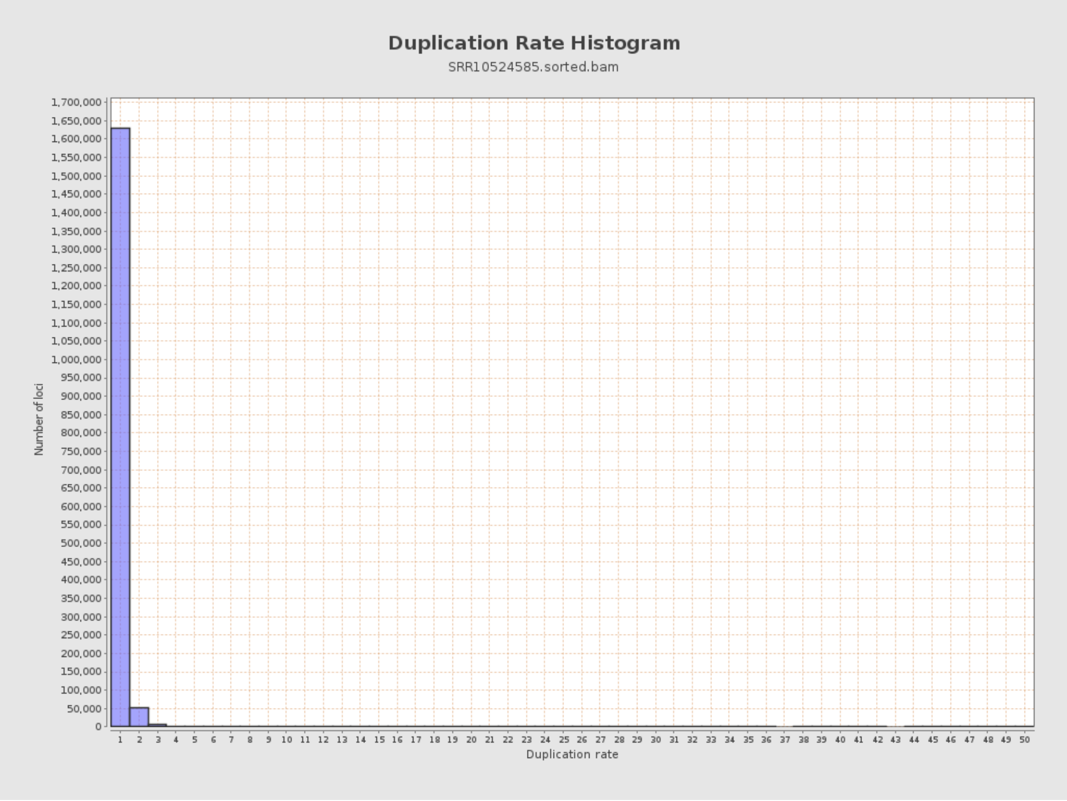
5. Results : Coverage Histogram (0-50X)



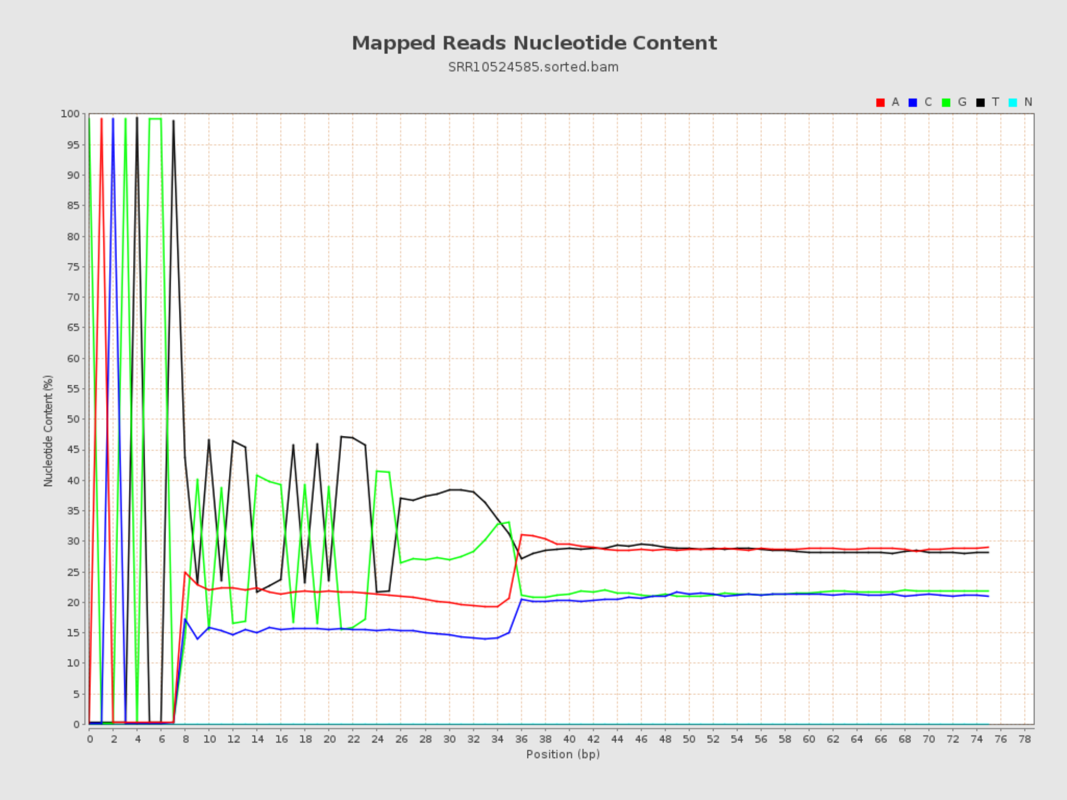
6. Results : Genome Fraction Coverage



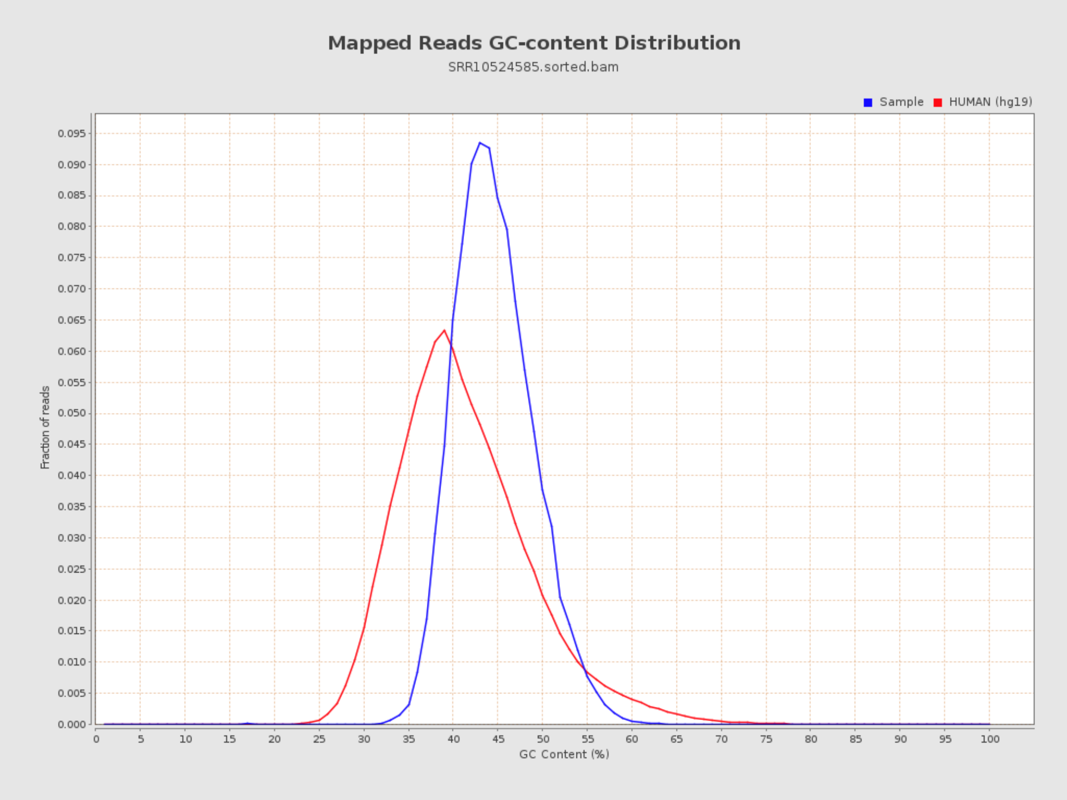
7. Results : Duplication Rate Histogram



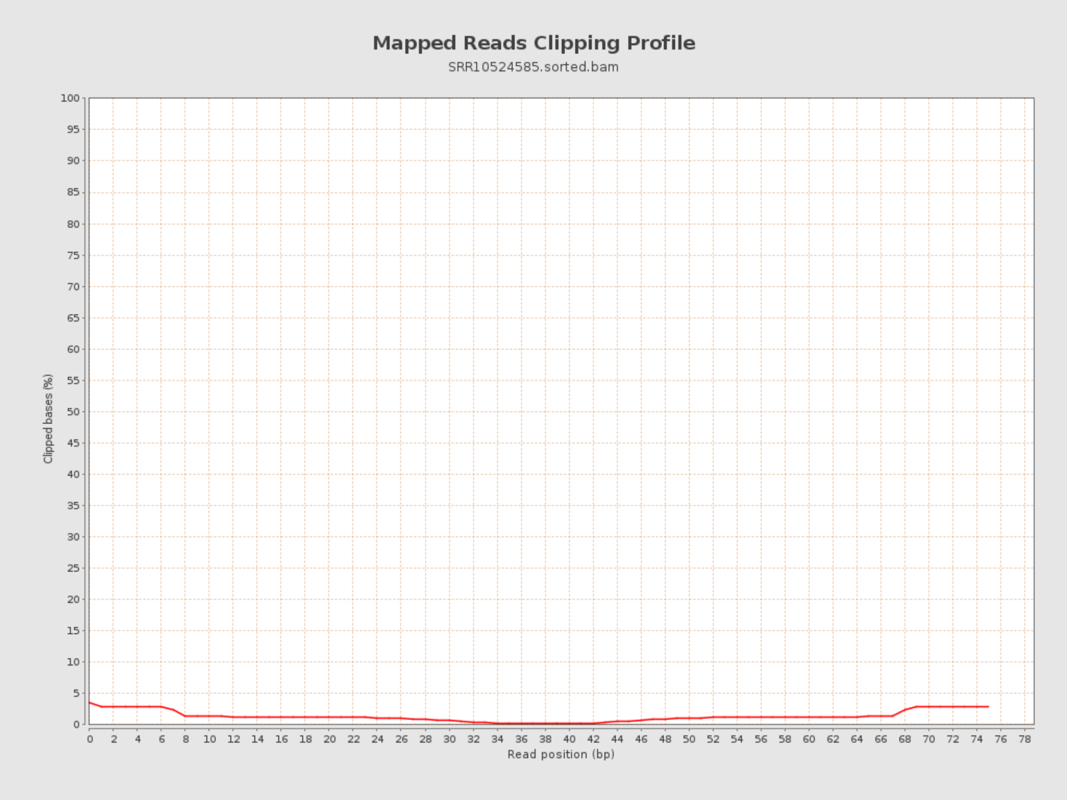
8. Results : Mapped Reads Nucleotide Content



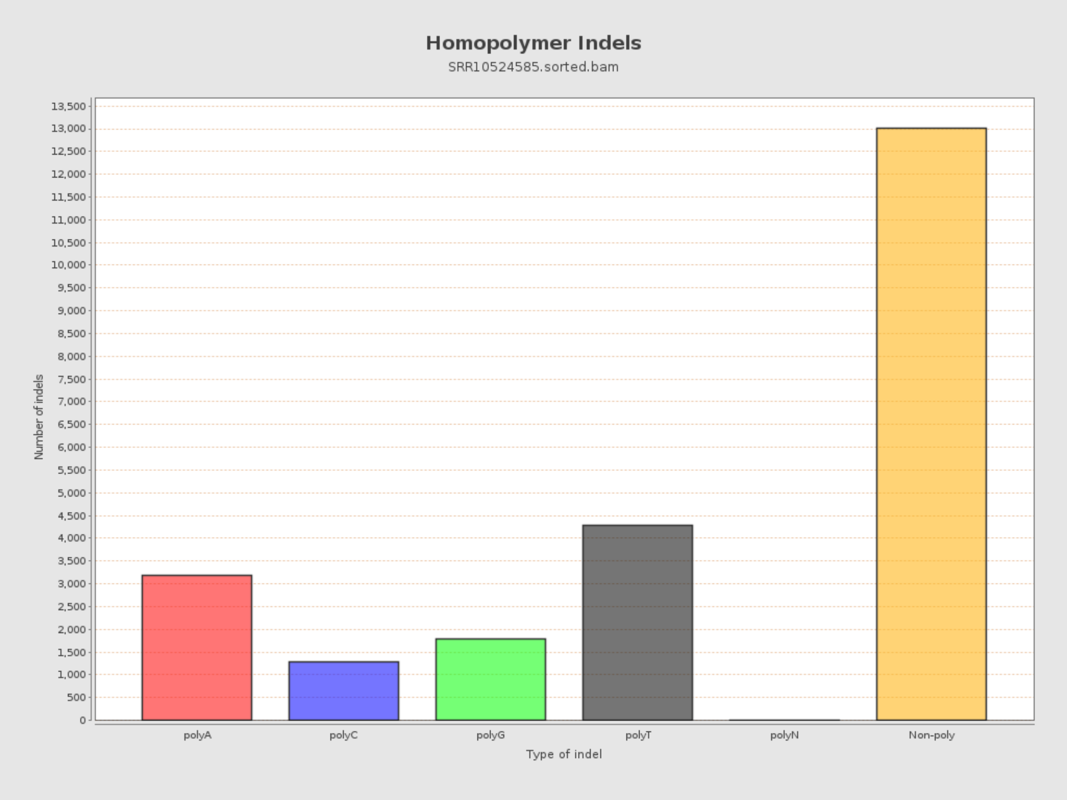
9. Results : Mapped Reads GC-content Distribution



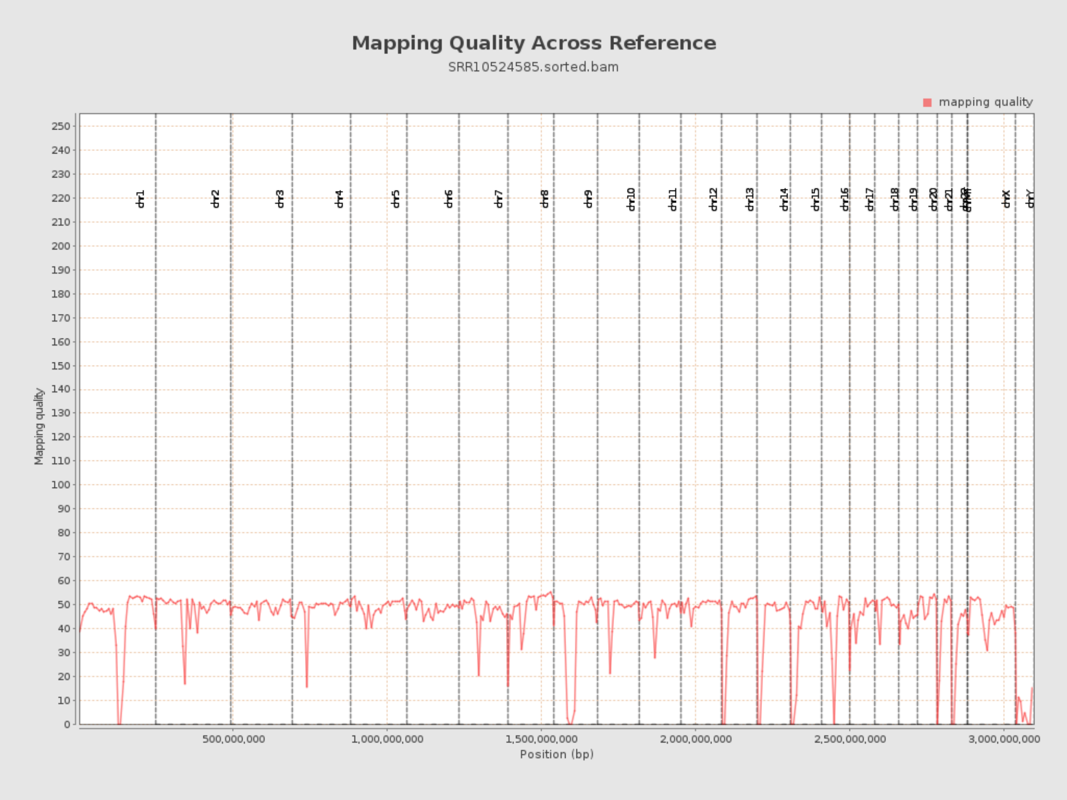
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram